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gga gaa gaa ctt ttc act gga gtt gtc cca att ctt gtt gaa tta gat   345
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
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Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
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Page 8

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gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc act act gga        441
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
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aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc tct tat ggt        489
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly
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gtt caa tgc ttt tcc cgt tat ccg gat cat atg aaa cgg cat gac ttt        537
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
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Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Ser
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Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
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gaa gat gga aac att ctc gga cac aaa ctc gag tac aac tat aac tca        729
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
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His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
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gac cat tat caa caa aat act cca att ggc gat ggc cct gtc ctt tta        873
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
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cca gac aac cat tac ctg tcg aca caa tct gcc ctt tcg aaa gat ccc        921
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
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Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys       Ile Pro
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Page 10

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
            35   40   45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50   55   60

Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65   70   75   80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85   90   95

Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
                100   105   110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
            115   120   125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130   135   140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145   150   155   160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165   170   175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
                180   185   190

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Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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Thr Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Gly Gly Thr Val Pro
                20                  25                  30

gta gaa aaa atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca     144
Val Glu Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
            35                  40                  45

att ctt gtt gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc     192
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
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Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
65                  70                  75                  80

ttt att tgc act act gga aaa cta cct gtt cca tgg cca aca ctt gtc     288
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
                85                  90                  95

act act ttc tct tat ggt gtt caa tgc ttt tcc cgt tat ccg gat cat     336
Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
                100                 105                 110

atg aaa cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta     384
Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
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Gln Glu Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
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gct gaa gtc aag ttt gaa ggt gat acc ctt gtt aat cgt atc gag tta     480
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
145                 150                 155                 160

aaa ggt att gat ttt aaa gaa gat gga aac att ctc gga cac aaa ctc     528
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
                    165                 170                 175

gag tac aac tat aac tca cac aat gta tac atc acg gca gac aaa caa     576
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
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aag aat gga atc aaa gct aac ttc aaa att cgc cac aac att gaa gat     624
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Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
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gag ttt gta act gct gct ggg att aca cat ggc atg gat gag ctc cgt     816
Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Arg
                    260                 265                 270

cga caa gct tgc ggc cgc act cga gca cca cca cca cca ctg aga         864
Arg Gln Ala Cys Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg
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Val Glu Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
        35                  40                  45


Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
    50                  55                  60


Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
65                  70                  75                  80


Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
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Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
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                     100                  105                     110
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    130   135   140

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Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
                165   170   175

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
                180   185   190

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
            195   200   205

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
    210   215   220

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
225   230   235   240

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
                245   250   255

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Arg
                260   265   270

Arg Gln Ala Cys Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg
        275   280   285

Ser Gly Cys
    290

<210>   8
<211>   17
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Frame adapter used for prevention of frameshift mutation as a
        result of plasmid modification

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<223>    Frame adapter used for prevention of frameshift mutation as a

         result of plasmid modification

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<210>    9
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<220>
<223>    Peptide design based on size and flexibility to act as a linker
         between the tag and GFP protein segments


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<221>    MISC_FEATURE
<223>    Peptide design based on size and flexibility to act as a linker
         between the tag and GFP protein segments

<400>    9

Met Gly Gly Thr Val
1               5


<210>    10
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<223>    Peptide design based on charge and shape to bind the

         expressed protein to a suitably interactive surface


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         expressed protein to a suitably interactive surface

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His His His His His His
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<210>    11
<211>    238
<212>    PRT
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<220>
<221>    MISC_FEATURE
<223>    Green fluorescent peptide coded by pGFPuv plasmid, permitting

easy visualisation and quantification based on fluorescence
properties

<400> 11

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
            35                  40                  45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
        50                  55                  60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
                100                 105                 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
            115                 120                 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180                 185                 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195                 200                 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210                 215                 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                 230                 235

<210> 12
<211> 291
<212> PRT
<213> Artificial sequence

<220>
<223> Completed peptide based on Hisx6 tag, short physically flexible
      linker and green fluorescent protein coded by pETM-GFP-Imm to
      impart fluorescence properties, allowing easy immobilisation with
      retention of bioactivity, visualisation and quantification


<220>
<221> MISC_FEATURE
<223> Completed peptide based on Hisx6 tag, short physically flexible
      linker and green fluorescent protein coded by pETM-GFP-Imm to
      impart fluorescence properties, allowing easy immobilisation with
      retention of bioactivity, visualisation and quantification

<400> 12

Met Lys His His His His His His Pro Met Ser Asp Tyr Asp Ile Pro
1               5                   10                  15


Thr Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Gly Gly Thr Val Pro
            20                  25                  30


Val Glu Lys Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
        35                  40                  45


Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
    50                  55                  60


Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
65                  70                  75                  80


Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
                85                  90                  95


Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
            100                 105                 110


Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
            115                 120                 125


Gln Glu Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
    130                 135                 140


Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
145                 150                 155                 160

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Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
                165             170             175

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
            180             185             190

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
            195             200             205

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
    210             215             220

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
225             230             235             240

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
            245             250             255

Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Arg
            260             265             270

Arg Gln Ala Cys Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg
            275             280             285

Ser Gly Cys
    290
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<210>  13
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<220>
<223>  Frame adapter

<400>  13

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